



PCT

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/889,733B

DATE: 04/15/2003
TIME: 13:51:10

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\04152003\I889733B.raw

2 <110> APPLICANT: VALLANCE, Patrick
3 LEIPER, James
4 WHITLEY, Guy
5 CHARLES, Ian
7 <120> TITLE OF INVENTION: DIMETHYLARGININE DIMETHYLAMINOHYDROLASES
9 <130> FILE REFERENCE: 117-358
11 <140> CURRENT APPLICATION NUMBER: US 09/889,733B
12 <141> CURRENT FILING DATE: 2001-09-14
14 <150> PRIOR APPLICATION NUMBER: GB 99017505.5
15 <151> PRIOR FILING DATE: 1999-01-26
16 <150> PRIOR APPLICATION NUMBER: GB 9913066.8
17 <151> PRIOR FILING DATE: 1999-06-04
19 <160> NUMBER OF SEQ ID NOS: 43
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 858
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(858)
32 <400> SEQUENCE: 1
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34 Met Ala Gly Leu Gly His Pro Ser Ala Phe Gly Arg Ala Thr His Ala
35 1 5 10 15
37 gtg gtg cg^g gcg cta ccc gag tcg ctc tgc cag cac g^c g^c ctg aga agc 96
38 Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser
39 20 25 30
41 gcc aag ggc gag gag gtg gac gtc gcc cg^c g^c gaa cg^g cag cac cag 144
42 Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln
43 35 40 45
45 ctc tac gtg ggc gtg ctg ggc agc aag ctg ggg ctg cag gtg gtg gag 192
46 Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu
47 50 55 60
49 ctg ccg gcc gac gag agc ctt ccg gac tgc gtc ttc gtg gag gac gtg 240
50 Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
51 65 70 75 80
53 gcc gtg gtg tgc gag gag acg gcc ctc atc acc cga ccc ggg g^c g^c ccg 288
54 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
55 85 90 95
57 agc cg^g agg aag gag gtt gac atg atg aaa gaa gca tta gaa aaa ctt 336
58 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
59 100 105 110

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61	cag	ctc	aat	ata	gta	gag	atg	aaa	gat	gaa	aat	gca	act	tta	gat	ggc	384	
62	Gln	Leu	Asn	Ile	Val	Glu	Met	Lys	Asp	Glu	Asn	Ala	Thr	Leu	Asp	Gly		
63				115				120							125			
65	gga	gat	gtt	tta	ttc	aca	ggc	aga	gaa	ttt	ttt	gtg	ggc	ctt	tcc	aaa	432	
66	Gly	Asp	Val	Leu	Phe	Thr	Gly	Arg	Glu	Phe	Phe	Val	Gly	Leu	Ser	Lys		
67				130				135							140			
69	agg	aca	aat	caa	cga	ggt	gct	gaa	atc	ttg	gct	gat	act	ttt	aag	gac	480	
70	Arg	Thr	Asn	Gln	Arg	Gly	Ala	Glu	Ile	Leu	Ala	Asp	Thr	Phe	Lys	Asp		
71	145				150				155						160			
73	tat	gca	gtc	tcc	aca	gtg	cca	gtg	gca	gat	ggg	ttg	cat	ttg	aag	agt	528	
74	Tyr	Ala	Val	Ser	Thr	Val	Pro	Val	Ala	Asp	Gly	Leu	His	Leu	Lys	Ser		
75					165				170						175			
77	ttc	tgc	agc	atg	gct	ggg	cct	aac	ctg	atc	gca	att	ggg	tct	agt	gaa	576	
78	Phe	Cys	Ser	Met	Ala	Gly	Pro	Asn	Leu	Ile	Ala	Ile	Gly	Ser	Ser	Glu		
79					180				185						190			
81	tct	gca	cag	aag	gcc	ctt	aag	atc	atg	caa	cag	atg	agt	gac	cac	cgc	624	
82	Ser	Ala	Gln	Lys	Ala	Leu	Lys	Ile	Met	Gln	Gln	Met	Ser	Asp	His	Arg		
83					195				200						205			
85	tac	gac	aaa	ctc	act	gtg	cct	gat	gac	ata	gca	gca	aac	tgt	ata	tat	672	
86	Tyr	Asp	Lys	Leu	Thr	Val	Pro	Asp	Asp	Ile	Ala	Ala	Asn	Cys	Ile	Tyr		
87					210				215						220			
89	cta	aat	atc	ccc	aaa	ggg	cac	gtc	ttg	ctg	cac	cga	acc	ccg	gaa		720	
90	Leu	Asn	Ile	Pro	Asn	Lys	Gly	His	Val	Leu	Leu	His	Arg	Thr	Pro	Glu		
91	225				230				235						240			
93	gag	tat	cca	gaa	agt	gca	aag	gtt	tat	gag	aaa	ctg	aag	gac	cat	atg	768	
94	Glu	Tyr	Pro	Glu	Ser	Ala	Lys	Val	Tyr	Glu	Lys	Leu	Lys	Asp	His	Met		
95					245				250						255			
97	ctg	atc	ccc	gtg	agc	atg	tct	gaa	ctg	gaa	aag	gtg	gat	ggg	ctg	ctc	816	
98	Leu	Ile	Pro	Val	Ser	Met	Ser	Glu	Leu	Glu	Lys	Val	Asp	Gly	Leu	Leu		
99					260				265						270			
101	acc	tgc	tgc	tca	gtt	tta	att	aac	aag	aag	gta	gac	tcc	tga			858	
102	Thr	Cys	Cys	Ser	Val	Leu	Ile	Asn	Lys	Lys	Val	Asp	Ser					
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107	<212>	TYPE:	PRT															
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110	<400>	SEQUENCE:	2															
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112	1				5				10						15			
115	Val	Val	Arg	Ala	Leu	Pro	Glu	Ser	Leu	Cys	Gln	His	Ala	Leu	Arg	Ser		
116					20				25						30			
118	Ala	Lys	Gly	Glu	Glu	Val	Asp	Val	Ala	Arg	Ala	Glu	Arg	Gln	His	Gln		
119					35				40						45			
121	Leu	Tyr	Val	Gly	Val	Leu	Gly	Ser	Lys	Leu	Gly	Leu	Gln	Val	Val	Glu		
122					50				55						60			
124	Leu	Pro	Ala	Asp	Glu	Ser	Leu	Pro	Asp	Cys	Val	Phe	Val	Glu	Asp	Val		
125					65				70						75			80
127	Ala	Val	Val	Cys	Glu	Glu	Thr	Ala	Leu	Ile	Thr	Arg	Pro	Gly	Ala	Pro		

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128	85	90	95
130	Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu		
131	100	105	110
133	Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly		
134	115	120	125
136	Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys		
137	130	135	140
139	Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp		
140	145	150	155
142	Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser		
143	165	170	175
145	Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu		
146	180	185	190
148	Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg		
149	195	200	205
151	Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr		
152	210	215	220
154	Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu		
155	225	230	235
157	Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met		
158	245	250	255
160	Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu		
161	260	265	270
163	Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser		
164	275	280	285
166	<210> SEQ ID NO: 3		
167	<211> LENGTH: 858		
168	<212> TYPE: DNA		
169	<213> ORGANISM: Homo sapiens		
171	<220> FEATURE:		
172	<221> NAME/KEY: CDS		
173	<222> LOCATION: (1)..(858)		
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176	atg ggg acg ccg ggg gag ggg ctg ggc cgc tgc tcc cat gcc ctg atc	48	
177	Met Gly Thr Pro Gly Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile		
178	1 5 10 15		
180	cgg gga gtc cca gag agc ctg gcg tcg ggg gaa ggt gcg ggg gct ggc	96	
181	Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly		
182	20 25 30		
184	ctt ccc gct ctg gat ctg gcc aaa gct caa agg gag cac ggg gtg ctg	144	
185	Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu		
186	35 40 45		
188	gga ggt aaa ctg agg caa cga ctg ggg cta cag ctg cta gaa ctg cca	192	
189	Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Glu Leu Pro		
190	50 55 60		
192	cct gag gag tca ttg ccg ctg gga ccg ctg ctt ggc gac acg gcc gtg	240	
193	Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val		
194	65 70 75 80		
196	atc caa ggg gac acg gcc cta atc acg cgg ccc tgg agc ccc gct cgt	288	

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197	Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg		
198	85	90	95
200	agg cca gag gtc gat gga gtc cgc aaa gcc ctg caa gac ctg ggg ctc		336
201	Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu		
202	100	105	110
204	cga att gtg gaa ata gga gac gag aac gcg acg ctg gat ggc act gac		384
205	Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp		
206	115	120	125
208	gtt ctc ttc acc ggc cggtt ttc gta ggc ctc tcc aaa tgg acc		432
209	Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr		
210	130	135	140
212	aat cac cga gga gct gag atc gtg gcg gac acg ttc cggtt gac ttc gcc		480
213	Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala		
214	145	150	155
216	gtc tcc act gtg cca gtc tcg ggt ccc tcc cac ctg cgc ggt ctc tgc		528
217	Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys		
218	165	170	175
220	ggc atg ggg gga cct cgc act gtt gtg gca ggc agc agc gac gct gcc		576
221	Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala		
222	180	185	190
224	caa aag gct gtc cgg gca atg gca gtg ctg aca gat cac cca tat gcc		624
225	Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala		
226	195	200	205
229	tcc ctg acc ctc cca gat gac gca gct gct gac tgt ctc ttt ctt cgt		672
230	Ser Leu Thr Leu Pro Asp Asp Ala Ala Asp Cys Leu Phe Leu Arg		
231	210	215	220
233	cct ggg ttg cct ggt gtg ccc ctt ctc ctg cac cgt gga ggt ggg		720
234	Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly		
235	225	230	235
237	240		
238	gat ctg ccc aac agc cag gag gca ctg cag aag ctc tct gat gtc acc		768
Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr			
239	245	250	255
241	ctg gta cct gtg tcc tgc tca gaa ctg gag aaa gct ggc gcc ggg ctc		816
242	Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu		
243	260	265	270
245	agc tcc ctc tgc ttg gtg ctc agc aca cgc ccc cac agc tga		858
246	Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser		
247	275	280	285
250	<210> SEQ ID NO: 4		
251	<211> LENGTH: 285		
252	<212> TYPE: PRT		
253	<213> ORGANISM: Homo sapiens		
255	<400> SEQUENCE: 4		
256	Met Gly Thr Pro Gly Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile		
257	1	5	10
259	15		
Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly			
260	20	25	30
262	Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu		
263	35	40	45

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265	Gly	Gly	Lys	Leu	Arg	Gln	Arg	Leu	Gly	Leu	Gln	Leu	Leu	Glu	Leu	Pro
266	50							55						60		
268	Pro	Glu	Glu	Ser	Leu	Pro	Leu	Gly	Pro	Leu	Leu	Gly	Asp	Thr	Ala	Val
269	65							70				75			80	
271	Ile	Gln	Gly	Asp	Thr	Ala	Leu	Ile	Thr	Arg	Pro	Trp	Ser	Pro	Ala	Arg
272								85				90			95	
274	Arg	Pro	Glu	Val	Asp	Gly	Val	Arg	Lys	Ala	Leu	Gln	Asp	Leu	Gly	Leu
275								100			105			110		
277	Arg	Ile	Val	Glu	Ile	Gly	Asp	Glu	Asn	Ala	Thr	Leu	Asp	Gly	Thr	Asp
278								115			120			125		
280	Val	Leu	Phe	Thr	Gly	Arg	Glu	Phe	Phe	Val	Gly	Leu	Ser	Lys	Trp	Thr
281								130			135			140		
283	Asn	His	Arg	Gly	Ala	Glu	Ile	Val	Ala	Asp	Thr	Phe	Arg	Asp	Phe	Ala
284	145							150			155			160		
286	Val	Ser	Thr	Val	Pro	Val	Ser	Gly	Pro	Ser	His	Leu	Arg	Gly	Leu	Cys
287								165			170			175		
289	Gly	Met	Gly	Gly	Pro	Arg	Thr	Val	Val	Ala	Gly	Ser	Ser	Asp	Ala	Ala
290								180			185			190		
292	Gln	Lys	Ala	Val	Arg	Ala	Met	Ala	Val	Leu	Thr	Asp	His	Pro	Tyr	Ala
293								195			200			205		
295	Ser	Leu	Thr	Leu	Pro	Asp	Asp	Ala	Ala	Asp	Cys	Leu	Phe	Leu	Arg	
296								210			215			220		
298	Pro	Gly	Leu	Pro	Gly	Val	Pro	Pro	Phe	Leu	Leu	His	Arg	Gly	Gly	
299	225							230			235			240		
301	Asp	Leu	Pro	Asn	Ser	Gln	Glu	Ala	Leu	Gln	Lys	Leu	Ser	Asp	Val	Thr
302								245			250			255		
304	Leu	Val	Pro	Val	Ser	Cys	Ser	Glu	Leu	Glu	Lys	Ala	Gly	Ala	Gly	Leu
305								260			265			270		
307	Ser	Ser	Leu	Cys	Leu	Val	Leu	Ser	Thr	Arg	Pro	His	Ser			
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321	Val	Pro	Ser	Lys	Lys	Ala	Leu	Val	Arg	Arg	Pro	Ser	Pro	Arg	Leu	Ala
322	1					5				10				15		
324	gaa	gga	ctg	gtg	aca	cac	gtc	gag	cgg	gag	cag	gtc	gat	cac	ggc	ctg
325	Glu	Gly	Leu	Val	Thr	His	Val	Glu	Arg	Glu	Gln	Val	Asp	His	Gly	Leu
326								20			25			30		
328	gcc	ctc	gaa	cag	tgg	gac	gcc	tac	gtc	gag	gcc	ctc	gga	gca	cac	ggc
329	Ala	Leu	Glu	Gln	Trp	Asp	Ala	Tyr	Val	Glu	Ala	Leu	Gly	Ala	His	Gly
330								35			40			45		
332	tgg	gag	act	ctg	gag	gtg	gac	ccg	gcc	gag	tac	tgt	ccg	gac	tcg	gtc
333	Trp	Glu	Thr	Leu	Glu	Val	Asp	Pro	Ala	Glu	Tyr	Cys	Pro	Asp	Ser	Val
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